Systems Biology Markup Language (SBML) Levels 2 and 3

***Hucka, Michael*[*1], *Finney, Andrew*[2], *Bornstein, Benjamin J.*[1], *Shapiro, Bruce E.*[1], *Doyle, John C.*[1], *Kitano, Hiroaki*[3]**

[1]California Institute of Technology, Pasadena, CA, USA; [2]University of Hertfordshire, Hatfield, Hertfordshire, UK; [3]The Systems Biology Institute, Tokyo, Japan

SBML is a machine-readable model definition language for representing biochemical networks. It is based upon XML, which in turn is a simple and portable text-based medium that is widely used in computational biology and bioinformatics. SBML's current vocabulary consists of structures for specifying fundamental aspects of a system of biochemical reactions, in particular the chemical species involved in the reactions, the reaction kinetics, the volumetric compartments in which the reactions take place, definitions of mathematical functions, parameters in the system, units on quantities, discrete events and delays, and additional mathematical constraints.

We continue to evolve SBML in cooperation with a community of software developers and modelers. Our approach has been to develop SBML in *level*s, where each higher level extends the set of features provided by lower levels of the language. In this poster, we provide an over-view of SBML with an emphasis on the main changes introduced in Level 2. These changes include: replacing SBML Level 1's text-string based format for mathematical formulas with MathML (a W3C standard), introducing support for metadata using the same scheme as CellML, introducing support for named function definitions, introducing explicit modifier species (e.g., catalysts) for reactions, and introducing new constructs for discrete events and time delays. We also describe two free software tools available under open-source licensing terms: libsbml, an SBML parser/writer library for Windows, Linux and MacOS intended to be embedded in applications, and MathSBML, a package for simulating and visualizing models in Mathematica.

Finally, we also discuss some of the features currently being developed for SBML Level 3. These include the ability to: (a) compose a model out of submodels, thus enabling the reuse of existing models; (b) have arrays of components allowing, for example, the description of tissues of cells; (c) describe spatial models including the shape of membranes and the rate of diffusion of species; (d) concisely describe the possible configurations of molecular complexes enabling, for example, the concise description of signaling pathway models; (e) supply a number of diagrammatic views of a model to enable the exchange of models between model visualization and drawing packages; and (f) label models with terms from standard controlled vocabularies so as to include relevant biological information in a model.

Software packages that support SBML today include: BASIS (University of Newcastle), CellDesigner (ERATO Kitano), Cellerator (JPL), Cytoscape (ISB), Exact Stochastic Simulator (University of Tennessee), Gepasi (Virginia Tech.), Jarnac (Keck Graduate Institute), Jdesigner (Keck Graduate Institute), JigCell (Virginia Tech.), BioSketchPad (BBN), MONOD (Molecular Sciences Institute), NetBuilder (University of Hertfordshire), SBW (Caltech and University of Hertfordshire), SigPath (Mount Sinai School of Medicine), StochSim (Cambridge University), TeraSim (Teranode Corporation), and Virtual Cell (UCHC). SBML is also the de facto model interchange standard used by the DARPA BioSPICE and IECA consortia. More information about SBML is available online at http://www.sbml.org.

The development of SBML has been funded by the Japan Science and Technology Corporation and the UK BBSRC.